User Manual for



make Pedigree file Version 1.2

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mPed User Manual

OVERVIEW AND PURPOSE

mPed is a program for converting pedigree data into an input file that can be used by the software PMx.

PMx – Population Management x (Ballou, J.D., Lacy, R.C. & Pollak, J.P., 2011. PMx: Software for Demographic and Genetic Analysis and Management of Pedigreed Populations (Version 1.0), Chicago Zoological Society, Brookfield, Illinois. http://www.vortex9.org/PMx.html) – is a free software developed for conservation genetic and demographic analyses and management of pedigreed zoo populations. PMx was designed to aid the management of populations for which the aim is to maintain the genetic diversity as close as possible to the source population over time.

PMx was developed as an accessory program to the Single Population Analysis and Records Keeping System (SPARKS; ISIS, 2005, User Manual for SPARKS, Version 1.5. ISIS, Eagan, USA. http://www2.isis.org/support/SPARKS/Pages/home.aspx) software for studbook record keeping. SPARKS is the international platform for zoo population studbooks. Input files for PMx are created by SPARKS. Today, more and more populations outside the zoo community are managed to maintain genetic diversity. This includes domestic breeds and wild animals for which pedigrees are available, and the management of these populations would benefit from being able to use PMx.

Although PMx can be used as a stand-alone program it requires preparation of an input file in a specific format (.ped, the PMx input file) which is complicated to create outside the SPARKS platform. Also, importing already existing studbooks into SPARKS is very difficult. Therefore, we developed the mPed (make ped file) converter program. mPed is written in the programming language C and can transform a studbook to a ped file that could be analyzed in PMx.

Necessary PMx input

The following information is the required minimum by PMx with respect to each animal:

Abbreviation used by PMx	<u>Explanation</u>
ID	Individual identification.
SireID	Identification of father (sire).
DamID	Identification of mother (dam).
Sex	$0 = female 1 = male^{1}$.
Selected	Individuals are selected to be included in the analysis. Two
	options are possible: $T - true / F - false$.
Dead	The animal is either dead $(T - true)$ or alive $(F - false)$.
Birth Date	Provide the date when the animal is born. Blank if
unknown.	
Death Date	Provide the date when the animal died. Blank if not dead
	or not known.
Location	Name of the place where the animal is located.
Local ID	Identification of location.
Other ID	Other ID (or individual information) that you want to add.
Otherib	Other 1D (of individual information) that you want to add.

In PMx you can add any additional fields that you wish to use to record further information about each animal, but these additional fields are not supported in mPed.

GETTING STARTED

System Requirements

mPed requires:

- RAM 256 MB or more.
- OS: Windows 7, Windows Vista or Windows XP (must have SP3), 32- or 64-bits.

Installation

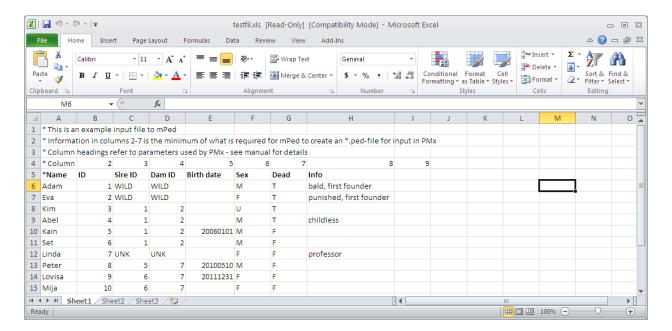
The mPed installation package can be downloaded from: www.popgen.su.se/mped.php This installation package should be saved in the local computer where it can be run.

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¹ For Vortex 1 = female 0 = male

The input file

The input file should be a tab-separated text file, and you need to transform your studbook data to this format. This can easily be done in e.g. MS Excel by choosing "Save as": Text (tab delimited) (*.txt). Example of studbook in MS Excel:



The same procedure works for other database programs. In MS Access, for example, you choose to export your data base with tab as delimiter.

If you want to make notes or comments in the input file you just put an asterisk (*) left of the note. An * is also needed before any headings if you have kept those in your text file.

RUN mPed

To run mPed you have to put your tab-separated text files in the same folder as you put the mped.exe and pedini.ini files (see instructions for the .ini file below).

To run mped.exe you double-click on the file and mPed runs, pedini.ini is read automatically. When finished, mPed writes "DONE". A screenshot of mPed:

```
C:\mPed\test\mped.exe

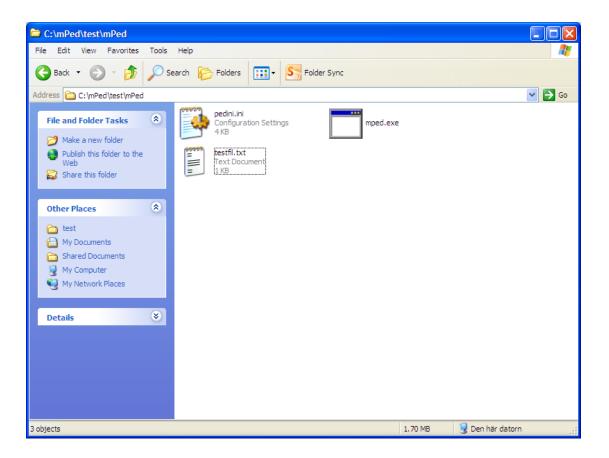
______
mPed = Make .ped file to PMx (v. 1.0) (Oct 23 2012) (02:18:57)

ini = (C:\mPed\test\pedini.ini)
Now running .................(C:\mPed\test\mped.exe)

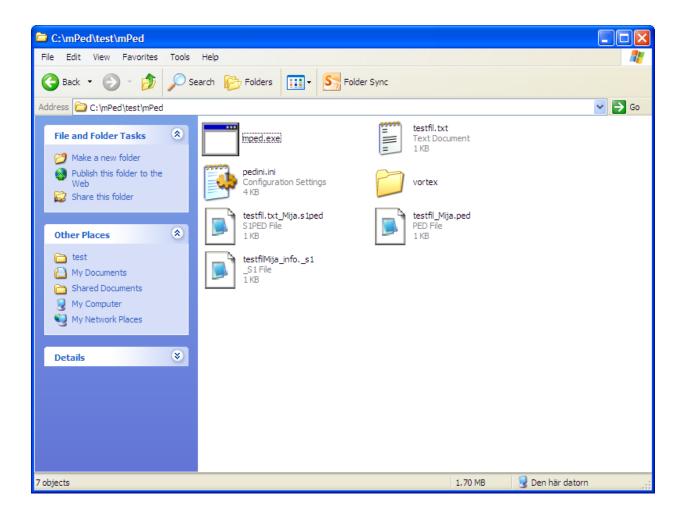
Ini=C:\mPed\test\pedini.ini
>>>>>>> DONE <<<<<<
```

Output files from mPed

Before the output files are created all your files are located in the same directory:



mPed generates a pedigree file for PMx (*.ped), a pedigree file for Vortex (*.txt) and one information file.



The output pedigree files are located in the same directory as your mped.exe, .ini, and .txt files, the file for Vortex is located in an directory of its own in the main directory. The .ped file can be run directly by PMx, and the .vortex file can be used directly by Vortex. (The Vortex file represents work in progress: we are currently working on generating an input file to the Vortex computer program.) Both PMx and Vortex can be downloaded free of charge from: http://www.vortex9.org/.

The information file

The first section contains information on the input data:

- Number of animals born certain years.
- Number of males/females.
- Number of unknown ancestors.

The second section of the file contains the same information for the result of running the pedigree through mPed.

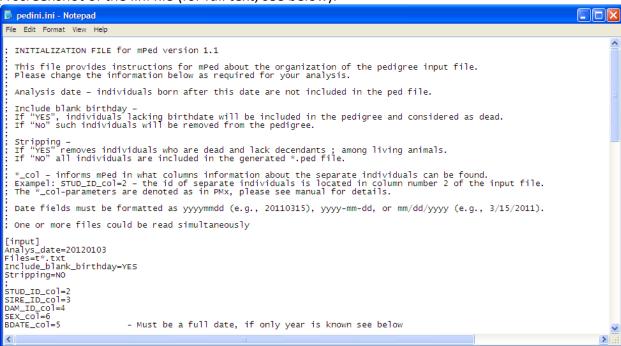
Check your *.ped-file

If you want to check your ped-file before running it through PMx, use for example MS Excel. a/ start MS Excel b/choose "Open" and file c/ choose "Delimited" d/ choose "Semicolon"

The mPED .ini file

mPed obtains instruction about the structure of the pedigree file (the tab delimited .txt file) and modifications needed from the .ini file. The .ini file is a text file in which the user changes and saves necessary instructions/information for mPed.

A screenshot of the .ini file (for full text, see below):



Explaining text, marked with semicolon (;) is automatically excluded when the program is executed.

Instructions to define the input file with pedini.ini:

- a) Open pedini.ini.
- b) The pedini.ini starts with stating the analysis date (for example 19951231). All individuals born after that date will be excluded from the file. (If all animals are to be included state today's date.)

- c) State path to the input file. If you want to run several files at once you can state an asterisk (*) in the file name, see example below.
 Files=D:\Mija_hundarMaj\h2011feb_ORIGINAL\h*.txt
 In this case every file that starts with an "h" in the folder will be analyzed.
- d) If you want to include individuals that lack birth date in the analysis, type: "YES" to include blank birth date, otherwise type "NO" to exclude individuals that lack birth date. (If you have animals that lack birth dates but that you know are alive we recommend that you first run the file through mPed and then manually change the dead T/F-column)
- e) mPed can remove unnecessary parts of the pedigree, i.e. lineages which are extinct because the ancestors do not have any living decendants, to make it easier to run PMx. Such removal of individuals is called "stripping". State "YES" or "NO" in the .ini file depending on if you want to strip off unnecessary individuals or not.
- f) Define from which column (the column number) in the input file the information/data should be collected. (E.g. "STUD_ID_col=2" means that your ID for each animal are placed in column two.) If you lack information for a certain column, just state "0". NB! If you are going to use "ONLY_SWEDISH_DOGS_ALIVE" set DEAD_col>0, even if you leave the fields blank.
- g) Define format for the animals' sex. For example "F" for female and "M" for male.
- h) [MIN_MAX_BIRTHDAY]: You can choose a latest possible and/or an earliest possible birth date of individuals if you want to make sure that erroneous <u>dates</u> in this respect are deleted (the individual will lack birthdate). "OLDEST_PARENT" states how much older than the offspring the parents are allowed to be. Dates that do not fit this condition will be removed. The format is YYMM; 2001 means 20 years and 1 month. (See function h) [MIN MAX BIRTHDAY] in the copy of the .ini file below.)
- i) [SIMULATED_DEATH_DATE]: State for how long an animal is assumed to live (for populations were death dates are not included).
- j) MAKE_BIRTHDAY: The function assumes the age of a parent based on its oldest offspring. For example, +2 results in parents being 2 years older than their oldest offspring, and the birth date is thus a date two years before the oldest offspring.
- k) COMMENT_IN_OUTPUT: YES or NO. Here you choose if you want comments on the output of mPed (including information on settings and number of individuals). PMx can handle this kind of comments but the older version of PMx – PM2000 – cannot.
- I) FILE_SUFFIX: You might add a suffix of maximum eight characters on your output file.

Date must be formatted as: yyyymmdd (e.g., 20110315), yyyy-mm-dd, or mm/dd/yyyy (e.g., 3/15/2011). These formats are supported in PMx. If you only have a year in your available

information, you have to make up and state the dates that should be added for PMx in, for example: Birthday_MMDD= 0307, Deathday_MMDD= 1008, because PMx demands full birthdays. (In PMx birth dates should be blank or complete.)

If you use several functions that exclude individuals from the output file, they are executed in the following order:

- 1. Analysis date
- 2. Stripping
- 3. Excluding individuals with blank birth date

Acknowledgement

Thanks to Mari Edman for help with usability testing of mPed and proofreading of this manual.

The ini file with user input marked in yellow

INCLUDE_BLANK_BIRTHDAY=YES

STRIPPING=NO

STUD_ID_COL=2 SIRE_ID_COL=17 DAM ID COL=18

SEX COL=4

```
; INITIALIZATION FILE for mPed version 1.2
; This file provides instructions for mPed about the organization of the pedigree input file.
; Please change the information below as required for your analysis.
; Analysis date – individuals born after this date are not included in the ped file.
; Include blank birthday -
; If "YES", individuals lacking birth date will be included in the pedigree and considered as dead.
; If "No" such individuals will be removed from the pedigree.
; Stripping -
; If "YES" removes individuals who are dead and lack descendants, among living animals.
; If "NO" all individuals are included in the generated *.ped file.
; * col – informs mPed in what columns information about the separate individuals can be found.
; Exampel: STUD_ID_col=2 – the id of separate individuals is located in column number 2 of the input
file.
; The *_col-parameters are denoted as in PMx, please see manual for details.
; Date fields must be formatted as yyyymmdd (e.g., 20110315), yyyy-mm-dd, or mm/dd/yyyy (e.g.,
3/15/2011).
; One or more files could be read simultaneously.
[INPUT]
ANALYSIS DATE=20101009
FILES=c:\mija \h*.txt
```

```
BDATE_COL=11
                       - Must be a full date, if only year is known see below
DEATHDATE_col=0
                       - Must be a full date, if only year is known see below
DEAD_COL=0
                       - T/F (True or False)
LOCATION_ID_COL=0 - Location (name of the place where the animal is kept)
LOCAL_ID_COL=2
                       - LocalID (ID at the place where the animal is kept)
OTHER_ID_COL=0
                       - OtherID (could be used for other IDs or other information about the animal)
; PMx needs a full birth date for each individual. If only year of birth is known, a full birth date must be
created.
; Provide the year of birth and death in columns entitled:
BDATEYYYY COL=0
                       - If only the year, and not the date, of birth is known.
DEATHDATEYYYY_COL=0
                               - If only the year, and not the date, of death is known.
; Provide a dummy date for birth and a dummy date for death
BIRTHDAY MMDD=0
DEATHDAY_MMDD=0
; Here the parameter value for sex is provided. Provide information on how you denote the sexes.
[format indata]
SEX SIRE=H
SEX DAM=T
SEX_UNK=U
[MIN_MAX_BIRTHDAY]
; If you want to make sure you spot erroneous birthdates and ages, provide the earliest possible date
; and/or the latest possible date that an individual within the pedigree can have been born.
; Oldest parent – provide the maximum age possible for a parent.
; (Only Swedish Dog Alive - (YES or NO) is a special parameter for data from the Swedish kennel club
stating to only include dogs registered in Sweden.
; i.e. registration number starting with S or SE.)
MIN BIRTHDAY=19000101
```

MAX BIRTHDAY=20211231

```
ONLY_SWEDISH_DOGS_ALIVE= NO
[SIMULATED_DEATH_DATE]
; Birthday to death - if information on death date is missing in your pedigree you can provide a
maximum age after which all individuals die.
; Make birthday – for individuals that lack birth dates and birth years and are parents –
; you can make dummy birthdate by providing information on the age (integers) of parents at first time
of reproduction.
; Example:
; +2 - parents are born two years prior to their first offspring.
; 0 - do not create dummy birthdates.
LONGEVITY=12
MAKE BIRTHDAY=+2
[COMMENTS]
; Comment_in_output – If "YES" information about the ini file is provided in the *.ped file
; File suffix - optional, if you want you can add an extension (maximum eight characters) to your file
name, e.g. pedigree_10.ped (where _10 is the extension)
; Local_ID & Other_ID - set these parameters to a set, same for all individual, optional value.
[data_default]
COMMENT IN OUTPUT=YES
FILE_SUFFIX=mija
LOCAL ID=optional
OTHER_ID=optional
```

OLDEST PARENT=14